

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 18:48:24 ; Search time 146.5 Seconds
(without alignments)
4196.184 Million cell updates/sec

Title: US-10-784-305-1
Perfect score: 1660
Sequence: 1.aggctaaagaagaaggggt.....atcatcatcatcatcattga 891

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delopt 7.0

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 2924198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cn2 1/USPTO spool p/US10784305/runat 31052005 182708 16649/app query.fasta_1.1031
-DB=Published Applications_AA -QFMT=fastan -SUFFIX=n2p.rapp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BL0SUM62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODES=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10784305 @CN2 1 1 199 @runat 31052005 182708 16649
-NCPUS=6 -ICPU=3 -NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: /cn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2: /cn2 6/ptodata/2/pubpaa/US06_PCT_NEW_PUB.pcp.*
3: /cn2 6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
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5: /cn2 6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
6: /cn2 6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
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8: /cn2 6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
9: /cn2 6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
10: /cn2 6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
11: /cn2 6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
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13: /cn2 6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
14: /cn2 6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
15: /cn2 6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
16: /cn2 6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
17: /cn2 6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
18: /cn2 6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
19: /cn2 6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
20: /cn2 6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pre. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	1317	79.3	622	15	US-10-378-832A-2	Sequence 2, Appl
2	1283	77.3	240	14	US-10-096-246-36	Sequence 36, Appl
3	1268	76.4	240	14	US-10-096-246-37	Sequence 37, Appl
4	1253	75.5	240	14	US-10-096-246-35	Sequence 35, Appl
5	1250	74.1	239	14	US-10-096-246-33	Sequence 33, Appl
6	1227.5	73.9	257	14	US-10-096-246-2	Sequence 2, Appl
7	1225	73.8	240	14	US-10-096-246-34	Sequence 34, Appl
8	1214	73.1	239	14	US-10-096-246-32	Sequence 32, Appl
9	1017.5	61.3	249	9	US-09-984-186-18	Sequence 18, Appl
10	1017.5	61.3	249	14	US-10-237-667-18	Sequence 18, Appl
11	1017.5	61.3	249	14	US-10-237-708-18	Sequence 18, Appl
12	1017.5	61.3	249	14	US-10-237-866-18	Sequence 18, Appl
13	1017.5	61.3	249	14	US-10-237-871-18	Sequence 18, Appl
14	1017.5	61.3	249	14	US-10-237-624-18	Sequence 18, Appl
15	1017.5	61.3	249	15	US-10-702-536-18	Sequence 18, Appl
16	1017.5	61.3	249	15	US-10-702-636-18	Sequence 18, Appl
17	938.5	56.5	264	14	US-10-114-716A-46	Sequence 46, Appl
18	932.5	56.2	331	14	US-10-059-261-169	Sequence 169, Appl
19	926.5	55.8	258	15	US-10-239-656-59	Sequence 59, Appl
20	911	54.9	262	15	US-10-336-210-4	Sequence 4, Appl
21	906.5	54.6	242	15	US-10-336-210-5	Sequence 5, Appl
22	902	54.3	444	14	US-10-013-173-49	Sequence 49, Appl
23	902	54.3	444	14	US-10-150-762-49	Sequence 49, Appl
24	902	54.3	444	14	US-10-244-821-49	Sequence 49, Appl
25	896	54.0	269	10	US-05-749-873-109	Sequence 109, Appl
26	892.5	53.8	288	15	US-10-363-349-7	Sequence 7, Appl
27	885.5	53.3	631	15	US-10-120-198B-2	Sequence 2, Appl
28	885	53.3	271	15	US-10-336-210-6	Sequence 6, Appl
29	884.5	53.3	272	15	US-10-336-210-7	Sequence 7, Appl
30	884	53.3	287	15	US-10-406-830-5	Sequence 5, Appl
31	884	53.3	533	15	US-10-257-864A-96	Sequence 96, Appl
32	884	53.3	533	15	US-10-221-131-101	Sequence 101, Appl
33	884	53.3	533	15	US-10-399-518-125	Sequence 125, Appl
34	883.5	53.2	274	14	US-10-138-505-32	Sequence 32, Appl
35	883.5	53.2	274	15	US-10-221-131-97	Sequence 97, Appl
36	883.5	53.2	271	15	US-10-399-518-121	Sequence 121, Appl
37	881.5	53.1	271	15	US-10-221-131-95	Sequence 95, Appl
38	881.5	53.1	274	14	US-10-138-505-26	Sequence 26, Appl
39	881.5	53.1	274	15	US-10-257-864A-90	Sequence 90, Appl
40	881.5	53.1	274	15	US-10-399-518-119	Sequence 119, Appl
41	877.5	52.9	244	9	US-09-940-391-1	Sequence 1, Appl
42	877.5	52.9	244	15	US-10-336-210-8	Sequence 8, Appl
43	875.5	52.7	274	15	US-10-257-864A-92	Sequence 92, Appl
44	874.5	52.7	243	17	US-10-879-994-10	Sequence 10, Appl
45	874.5	52.7	243	17	US-10-610-452-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-378-832A-2
Sequence 2, Application US/10378832A
Publication No. US20040005333A1
GENERAL INFORMATION:

APPLICANT: Her Majesty the Queen in right of Canada, as represented by the Minister
of National Defence
APPLICANT: Nagata, Leslie P
APPLICANT: Fulton, R. Elaine
APPLICANT: Hu, Weigang
APPLICANT: Alvi, Azhar Z
TITLE OF INVENTION: No. US20040005333A1el Fusion Protein of Human IgG1 Heavy Chain Co
TITLE OF INVENTION: Antibody Against Venezuelan Equine Encephalitis Virus
FILE REFERENCE: NEU-0013
CURRENT APPLICATION NUMBER: US/10/378,832A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 622
TYPE: PRT
ORGANISM: mouse hybridoma cells and human lymphocytes

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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 18:45:54 ; Search time 36.5 Seconds
(without alignments)
3644.510 Million cell updates/sec

Title: US-10-784-305-1

Perfect score: 1660

Sequence: 1 atggctaaagaaggggt.....atcatcatcatcatcattga 891

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Zgapop 6.0 , Zgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DRV=xlp

-Q=/cgn2_1/USFTO_spool_9/US10784305/runat_31052005_182708_16626/app_query.fasta_1.1031

-DB=Issued Patents AA -QFW=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPEL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US10784305@cgn 1.1 46 @runat_31052005_182708_16626 -NCFU=6 -ICPU=3

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*

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5: /cgn2_6/ptodata/1/iaa/PCPTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1283	77.3	240	4	US-10-092-246-36
2	1283	77.3	240	4	US-10-096-246A-37
3	1275	76.8	240	4	US-10-096-246A-36
4	1268	76.4	240	4	US-10-092-246-37
5	1258	75.8	240	4	US-10-096-246A-35
6	1253	75.5	240	4	US-10-092-246-35
7	1230	74.1	239	4	US-10-092-246-33
8	1230	74.1	239	4	US-10-096-246A-33
9	1230	74.1	240	4	US-10-096-246A-34
10	1227.5	73.9	257	4	US-10-092-246-2
11	1227.5	73.9	257	4	US-10-096-246A-2
12	1225	73.8	240	4	US-10-092-246-34

13	1214	73.1	239	4	US-10-092-246-32	Sequence 32, Appl
14	1214	73.1	239	4	US-10-096-246A-32	Sequence 32, Appl
15	1017.5	61.3	249	4	US-08-797-689-18	Sequence 18, Appl
16	1017.5	61.3	249	4	US-09-984-186-18	Sequence 18, Appl
17	952.5	57.4	288	3	US-09-423-439-38	Sequence 38, Appl
18	938.5	56.5	673	3	US-09-423-439-32	Sequence 32, Appl
19	916	55.2	273	2	US-08-403-853-18	Sequence 18, Appl
20	902.5	54.0	355	3	US-08-875-811-57	Sequence 57, Appl
21	896	54.0	269	3	US-08-646-265A-109	Sequence 109, App
22	889.5	53.6	297	4	US-09-486-814A-2	Sequence 2, Appl1
23	877.5	52.9	244	4	US-09-244-369B-1	Sequence 1, Appl1
24	877.5	52.9	244	4	US-09-940-391-1	Sequence 1, Appl1
25	871	52.5	267	3	US-09-485-737B-2	Sequence 2, Appl1
26	862	51.9	637	1	US-10-071-485-2	Sequence 2, Appl1
27	862	51.9	637	1	US-08-235-838-14	Sequence 14, Appl
28	861	51.9	530	4	US-08-465-473B-14	Sequence 14, Appl
29	861	51.9	530	4	US-08-840-713-2	Sequence 2, Appl1
30	861	51.9	711	1	US-08-235-838-7	Sequence 7, Appl1
31	861	51.9	711	2	US-08-465-473B-7	Sequence 7, Appl1
32	859	51.7	615	4	US-08-840-713-35	Sequence 35, Appl
33	859	51.7	617	4	US-08-840-713-37	Sequence 37, Appl
34	855.5	51.5	301	2	US-08-661-052-14	Sequence 14, Appl
35	855.5	51.5	301	3	US-09-188-082-14	Sequence 14, Appl
36	855.5	51.5	301	3	US-09-364-088-14	Sequence 14, Appl
37	855.5	51.5	301	3	US-09-102-716-14	Sequence 14, Appl
38	855	51.5	241	1	US-08-235-838-5	Sequence 5, Appl1
39	855	51.5	241	2	US-08-465-473B-5	Sequence 5, Appl1
40	853	51.4	239	3	US-08-279-772A-8	Sequence 8, Appl1
41	853	51.4	239	3	US-08-902-486-11	Sequence 11, Appl
42	847.5	51.1	599	1	US-08-463-163-3	Sequence 3, Appl1
43	845	50.9	637	2	US-08-235-838-16	Sequence 16, Appl
44	845	50.9	637	2	US-08-465-473B-16	Sequence 16, Appl
45	839	50.5	541	3	US-09-485-737B-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1

US-10-092-246-36

; Sequence 36, Application US/10092246

; Patent No. 6501314

; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R B

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leelie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of a

; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/092,246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1

US-10-092-246-36

Alignment Scores:

Pred. No.: 2,72e+103 Length: 240

Score: 1283.00 Matches: 240

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 77.29% Indels: 0

DB: 4 Gaps: 0

US-10-784-305-1 (1-891) x US-10-092-246-36 (1-240)

QY 76 ATGGCCAGGTCTCACTGAGGAGTCAAGCTGAGCTGGTGGAGCTGGGCTTCAGTG 135

Db 1 MetAlaInValGlnleuGlnGluSerGlyProGluLeuValysProGlyAlaSerVal 20

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 18:44:54 ; Search time 192 Seconds
(without alignments)

4752.735 Million cell updates/sec

Title: US-10-784-305-1

Perfect score: 1660

Sequence: 1 atggctaagaagaaggggt.....atcatcatcatcatcattga 891

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DRV=xlp
-Q=/cgn2_1/USFTO.spool_p/US10784305/runat_31052005_182707_16603/app.query.fasta_1.1031
-DB=Uniprot -QFWT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10784305_@CEN_1_1_244_@runat_31052005_182707_16603 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	883	53.2	243	2 Q7TQM2	Q7tqm2.mus musculus
2	831	50.1	244	2 Q65ZC8	Q65zc8.homo sapien
3	823	49.6	255	2 Q6KB05	Q6kb05.mus musculus
4	808	48.7	487	2 Q65ZL2	Q65zl2.mus sp. fv/
5	795	47.9	240	2 Q65ZC9	Q65zc9.homo sapien
6	774	46.6	298	2 Q9QIF0	Q9qif0.synthetic c
7	769	46.3	241	2 Q921A6	Q921a6.mus musculus
8	742.5	44.7	248	2 Q65ZQ7	Q65zq7.mus sp. b3{
9	639.5	38.5	218	2 Q925S1	Q925s1.mus musculus
10	512.5	30.9	170	2 Q925S2	Q925s2.mus musculus
11	469	28.3	481	2 Q91WT1	Q91wt1.mus musculus
12	464	28.0	473	2 Q9DBL4	Q9dbl4.mus musculus
13	457	27.5	465	2 Q6PJB2	Q6pjb2.mus musculus
14	454.5	27.4	613	2 Q8VCX7	Q8vcx7.mus musculus
15	445.5	26.8	464	2 Q6PP95	Q6pp95.mus musculus
16	445	26.8	142	2 Q924Q1	Q924q1.mus musculus

17	444	26.7	614	2 Q7TMT6	Q7tmt6.mus musculus
18	443.5	26.7	472	2 Q6PJA7	Q6pja7.mus musculus
19	441.5	26.6	143	2 Q924P9	Q924p9.mus musculus
20	441	26.6	134	2 Q65ZB6	Q65zb6.mus musculus
21	440.5	26.5	143	2 Q924Q0	Q924q0.mus musculus
22	440	26.5	140	2 Q924P8	Q924p8.mus musculus
23	439.5	26.5	139	1 HV07 MOUSE	P01751.mus musculus
24	437.5	26.4	482	2 Q8KL72	Q8kl72.mus musculus
25	435	26.2	140	2 Q924R2	Q924r2.mus musculus
26	435	26.2	463	2 Q99LC4	Q99lc4.mus musculus
27	434.5	26.2	145	2 Q924Q9	Q924q9.mus musculus
28	434	26.1	146	2 Q924Q3	Q924q3.mus musculus
29	433.5	26.1	143	2 Q91V67	Q91v67.mus musculus
30	433.5	26.1	145	2 Q924Q6	Q924q6.mus musculus
31	433.5	26.1	145	2 Q924R1	Q924r1.mus musculus
32	433	26.1	480	2 Q8KQZ4	Q8kqz4.mus musculus
33	432.5	26.1	143	2 Q924R0	Q924r0.mus musculus
34	432.5	26.1	145	2 Q924R4	Q924r4.mus musculus
35	432	26.0	142	2 Q924Q2	Q924q2.mus musculus
36	431.5	26.0	137	2 Q924R6	Q924r6.mus musculus
37	431	26.0	147	2 Q925S3	Q925s3.mus musculus
38	430.5	25.9	137	1 HV11 MOUSE	P01755.mus musculus
39	430	25.9	117	2 Q9QXB9	Q9qxb9.mus musculus
40	430	25.9	146	2 Q924R8	Q924r8.mus musculus
41	430	25.9	470	2 Q7TMM1	Q7tmm1.mus musculus
42	428.5	25.8	145	2 Q924P7	Q924p7.mus musculus
43	428	25.8	108	2 Q8VJ30	Q8vj30.mus musculus
44	428	25.8	140	1 HV02 MOUSE	P01746.mus musculus
45	427.5	25.8	145	2 Q924Q7	Q924q7.mus musculus

ALIGNMENTS

RESULT 1

Q7TQM2 ID Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2; Q7TQM2 (TREMELREL. 25, Created)
DT 01-OCT-2003 (TREMELREL. 25, Last sequence update)
DT 01-OCT-2003 (TREMELREL. 26, Last annotation update)
DT 01-MAR-2004 (TREMELREL. 26, Last annotation update)
DB ScFv 6H8 protein (Fragment)
GN Name=scFv 6H8;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Btekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor";
RL J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -;
DR HSSP; P01751; IAGW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
PT NON_TER
SQ SEQUENCE 243 AA; 25976 MW; B5PFF64D2DCFAF76 CRC64;

Alignment Scores:

Pred. No.: 1,15e-64 Length: 243
Score: 883.00 Matches: 168
Percent Similarity: 74.07% Conservative: 32
Best Local Similarity: 62.22% Mismatches: 42
Query Match: 53.19% Indels: 28
DB: 2 Gaps: 3

US-10-784-305-1 (1-891) x Q7TQM2 (1-243)

1	825.5	49.7	268	2	A56446	Ig heavy chain V r
2	792.5	47.7	249	2	S41374	single chain Fv an
3	715.5	43.1	233	2	JC5322	p53 specific singl
4	526	31.7	469	2	S37483	Ig gamma-2a chain
5	517.5	31.2	246	2	S38950	Ig gamma chain - m
6	517.5	31.2	446	2	S40295	Ig gamma-2a chain
7	495	29.8	144	2	B30502	Ig heavy chain V r
8	494	29.8	117	2	S42466	Ig kappa chain V r
9	487	29.3	131	2	PL0207	anti-idiotypic ant
10	487	29.3	138	2	S21810	Ig heavy chain V r
11	475	28.6	138	2	B32513	Ig heavy chain pre
12	471.5	28.4	115	2	A54378	Ig heavy chain V r
13	469	28.3	136	2	P02008	Ig heavy chain pre
14	468.5	28.2	135	2	A30577	Ig heavy chain pre

```

Copyri
OM nucleic - protein sear
Run on:      May 31,
Title:       US-10-78
Perfect score: 1660
Sequence:    1 atggcgc
Scoring table:
              BLOSUM62
              Xgapop 1
              Ygapop 1
              Fgapop
              Delop
Searched:    283416 s
Total number of hits sat
Minimum DB seq length: 0
Maximum DB seq length: 2
Post-processing: Minimum
                  Maximum
                  Listing

```

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 31, 2005, 18:35:52 ; Search time 159.5 Seconds
(without alignments)
4321.047 Million cell updates/sec

Title: US-10-784-305-1
Perfect score: 1660
Sequence: 1 aaggctaagaagaaggggt.....atcatcatcatcatcattga 891

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q/cn2 1/USFTO spool_p/US10784305/runat 31052005 182706 16596/app query fasta_1.1031
-DB=A_Geneseq -QFWT=fastan -SUPPIX=n2p.rag -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10784305 @CN 1.1 224 @runat 31052005 182706 16596 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: Geneseq19808:*
2: Geneseq19908:*
3: Geneseq20008:*
4: Geneseq20018:*
5: Geneseq20028:*
6: Geneseq20038:*
7: Geneseq20038a:*
8: Geneseq20048a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1602	96.5	296	ADS20752	ADS20752 SBP tagge
2	1283	77.3	240	ABU07883	ABU07883 Venezuela
3	1275	76.8	240	ABU07882	ABU07882 Venezuela
4	1258	75.8	240	ABU07881	ABU07881 Venezuela
5	1230	74.1	239	ABU07879	ABU07879 Venezuela
6	1230	74.1	240	ABU07880	ABU07880 Venezuela
7	1227.5	73.9	257	ABU07877	ABU07877 Anti-Vene
8	1084	65.3	283	ADR5426	ADR5426 V1228CFV
9	962	59.2	269	ADR28054	ADR28054 NPB Polyp
10	960	57.8	267	ADR70320	ADR70320 Polioviru

11	954.5	57.5	240	6	ABJ26742	Abj26742 VEGF bind
12	954.5	57.5	240	8	ADK18245	Adk18245 Mouse VEG
13	952.5	57.4	288	2	AAW82743	Aaw82743 Fusion pr
14	950.5	57.3	577	4	AAI19872	Aai19872 Activatin
15	945.5	57.0	555	4	AAI19871	Aai19871 Activatin
16	945.5	57.0	565	4	AAI19873	Aai19873 Activatin
17	943	56.8	260	8	ADL65425	Adl65425 DNA gyrae
18	941.5	56.7	704	4	AAI19888	Aai19888 MLV envel
19	941	56.7	248	2	AAW58836	Aaw58836 Human CD3
20	938.5	56.5	264	6	ABG72735	Abg72735 Mouse rec
21	938.5	56.5	673	3	AAW82742	Aaw82742 Plasmid p
22	938	56.5	305	3	AAV51142	Aav51142 Murine de
23	938	56.5	305	3	AAV59265	Aav59265 Antibody
24	926.5	55.8	258	5	AAU72865	Aau72865 PS-2 sing
25	925.5	55.8	330	4	AAU70842	Aau70842 SNV-env 1
26	925.5	55.8	580	2	AAW90217	Aaw90217 Bispecifi
27	917.5	55.3	309	4	AAW70841	Aaw70841 SNV-env 1
28	917	55.2	392	3	AAI10863	Aai10863 S11-VRGP2
29	916	55.2	273	3	AAI10864	Aai10864 S11-scVEG
30	916	55.2	510	3	AAI10865	Aai10865 Anti-inf1
31	914	55.1	244	8	ADG17485	Adg17485 Anti-CD22
32	913	55.0	244	8	ADG17477	Adg17477 Anti-CD22
33	911	54.9	244	8	ADG17479	Adg17479 Anti-CD22
34	911	54.9	244	8	ADG17480	Adg17480 Anti-CD22
35	911	54.9	262	4	AAI1421	Aai1421 Protein u
36	910	54.8	244	8	ADG17478	Adg17478 Anti-CD22
37	909	54.8	244	8	ADG17487	Adg17487 Anti-CD22
38	908	54.7	244	8	ADG17476	Adg17476 Anti-CD22
39	908	54.7	244	8	ADG17484	Adg17484 Anti-CD22
40	906.5	54.6	242	4	AAI1422	Aai1422 Protein u
41	906	54.6	244	8	ADG17483	Adg17483 Anti-CD22
42	906	54.6	543	7	ADD12876	Add12876 CD28/mela
43	905	54.5	697	8	ADG17482	Adg17482 Anti-CD22
44	904.5	54.5	697	8	ADQ07403	Adq07403 hCBEL1/hB
45	904.5	54.5	697	8	ADQ12180	Adq12180 Heavy cha

ALIGNMENTS

RESULT 1
ADS20752
ID ADS20752 standard; protein; 296 AA.
XX
AC ADS20752;
XX
DT 18-NOV-2004 (first entry)
XX
DE SBP tagged recombinant scFv fusion protein, seq id 2.
XX
KW Single-chain variable fragment antibody; scFv Ab;
KW streptavidin-binding peptide; SBP; fusion protein;
KW anti-Venezuelan equine encephalitis virus; VEE; mouse.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Protein 1..269
FT /label= scFv
FT Region 270..296
FT /note= "SBP, 6His and spacers"
XX
CA2458824-A1.
XX
PD 24-AUG-2004.
XX
PF 24-FEB-2004; 2004CA-02458824.
XX
PR 24-FEB-2003; 2003US-0448902P.
XX
PA (MIND) CANADA MIN NAT DEFENCE.
XX
PI Nagata LP, Fulton RE, Hu W, Alvi AZ;
XX